Amendments to Claims

Claims 1-23 (Canceled)

Claim 24 (Currently Amended) A method for the production of single cell protein comprising:

(a) providing a high growth methanotrophic bacterial strain which:

(1) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and

(2) comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate dependent phosphofructokinase enzyme, the gene selected from the group consisting of:

(i) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:6; and

(ii) an isolated nucleic acid molecule that hybridizes with (a) when washed with 0.1X SSC, 0.1% SDS, 65°C;

ba) contacting the bacterial strains of ~~any of the Claims 1, 2, 3, 5, or 18~~ (a)with C1 carbon substrate, selected from the group consisting of methane and methanol, in a suitable medium for a time sufficient to permit the expression and accumulation of single cell protein; and

c~~b~~) optionally recovering the single cell protein.

Claim 25 (Currently Amended) . The method of Claim ~~23~~ 24 wherein the C1 carbon substrate is contacted with the bacterial strain under anaerobic conditions.

Claim 26 (Currently Amended). The method of Claim ~~23~~ 24 wherein the C1 carbon substrate is contacted with the bacterial strain under aerobic conditions.

Claim 27 (Canceled).

Claim 28 (Currently Amended). A method for the production of a feed product comprising protein, carbohydrates and pigment comprising the steps of:

(a) providing a high growth methanotrophic bacterial strain which:

(1) grows on a C1 carbon substrate selected from the group consisting of methane and methanol; and

(2) comprises a functional Embden-Meyerhof carbon pathway, said pathway comprising a gene encoding a pyrophosphate dependent phosphofructokinase enzyme, the gene selected from the group consisting of:

(i) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:6; and

(ii) an isolated nucleic acid molecule that hybridizes with (a) when washed with 0.1X SSC, 0.1% SDS, 65°C;

b~~a~~) contacting the bacterial strain ~~of any of Claims 1, 2, 3, 5 or 18~~(a) with a C1 carbon substrate in a suitable medium for a time sufficient to permit the expression and accumulation of the feed product; and

c~~b~~) optionally recovering the feed product.

Claim 29(Original). A method according to Claim 28 wherein the relative compositions of protein, carbohydrate and pigment are altered through the up-regulation or down-regulation of any one of the genes encoding the proteins selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, and 69.

Claim 30 (Currently Amended). A method of identifying ~~the~~ a high growth methanotrophic bacterial ~~strain of Claim 1~~ comprising:

(a) growing a sample suspected of containing a high growth methanotrophic bacterial strain on a suitable growth medium in the presence of methane as a sole carbon source;

(b) identifying colonies that grow on the conditions of step (a);

(c) analyzing the colonies identified in step (b) for the presence of pyrophosphate dependent phosphofructokinase activity.

Claim 31 (Currently Amended). A method according to Claim 30 wherein the colonies of step (b) are additionally analyzed for the presence of a gene selected from the group consisting of:

(a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:6;

(b) an isolated nucleic acid molecule that hybridizes with (a) ~~under the following hybridization conditions:~~when washed with 0.1X SSC, 0.1% SDS, 65°C ~~and washed with 2X SSC, 0.1% SDS followed by 0.1X SSC, 0.1% SDS~~;

~~(c) an isolated nucleic acid molecule comprising a first nucleotide sequence encoding a polypeptide of at least 437 amino acids that has at least 63% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:6;~~ and

(c~~d~~) an isolated nucleic acid molecule that is complementary to (a), or (b). ~~or (c).~~

Claim 32 (Original). A method for the production of single cell protein comprising:

a) providing a high growth methanotrophic bacterial strain comprising a functional Embden-Meyerhof pathway;

b) contacting the bacterial strain of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby single cell protein is produced; and

c) optionally recovering the single cell protein.

Claim 33 (Original). A method for the production of production of a feed product comprising protein, carbohydrates and pigment comprising:

a) providing a high growth methanotrophic bacterial strain comprising a functional Embden-Meyerhof pathway;

b) contacting the bacterial strain of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby the feed product is produced; and

c) optionally recovering the feed product.

Claim 34 (Original) A method for the production of production of exopolysaccharides comprising:

a) providing a high growth methanotrophic bacterial strain comprising a functional Embden-Meyerhof pathway;

b) contacting the bacterial strain of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby exopolysaccharides are produced; and

c) optionally recovering the exopolysaccharides.

Claim 35 (Original). A method according to anyone of Claims 32-34 wherein the functional Embden-Meyerhof pathway contains a gene encoding a pyrophosphate dependent phosphofructokinase enzyme.

Claim 36 (Original). A method according to anyone of Claims 32-34 wherein the C1 substrate is selected from the group consisting of methane, methanol, formaldehyde, formic acid, methylated amines, and methylated thiols.